

Fig. 1

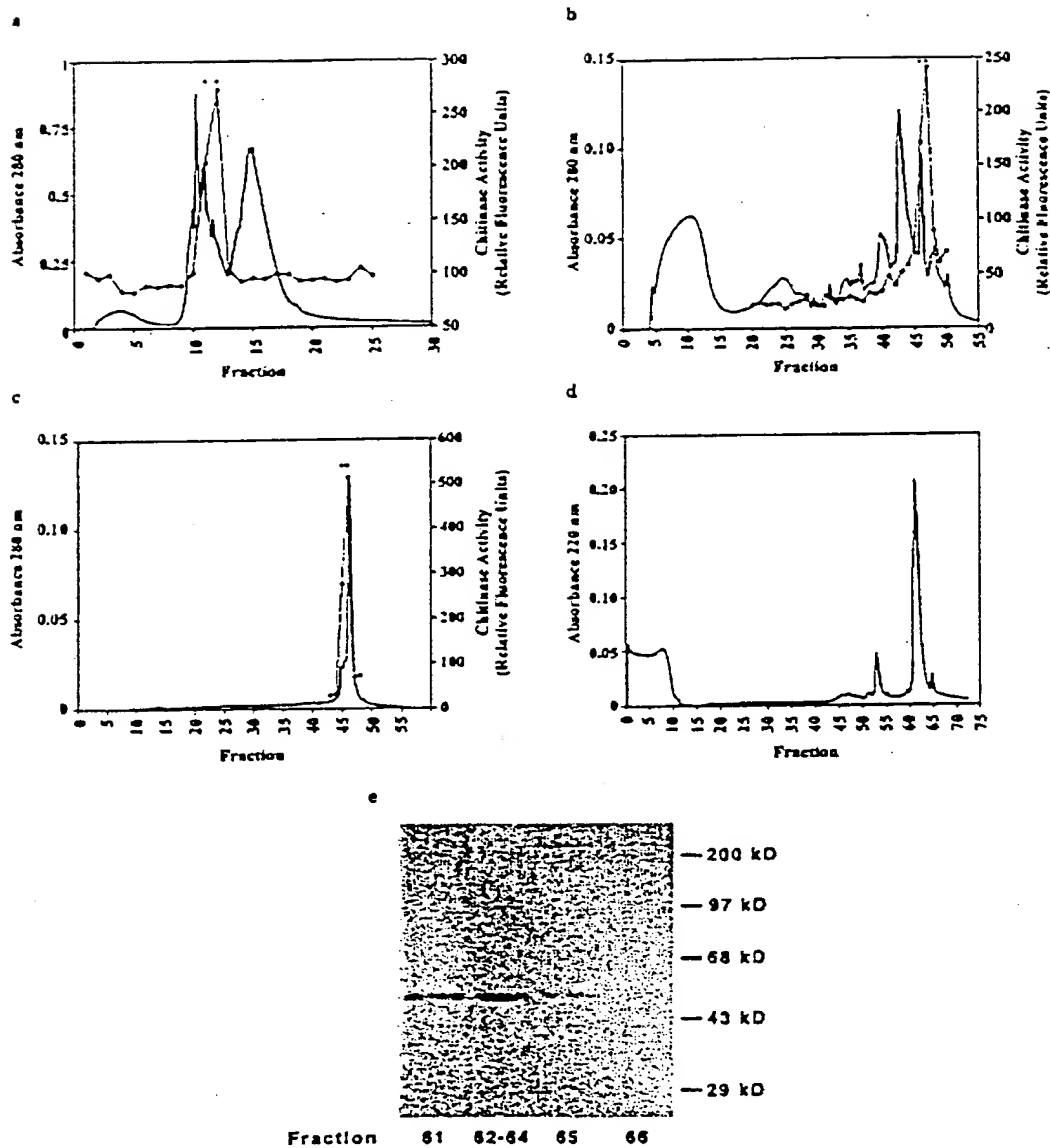


Fig. 2

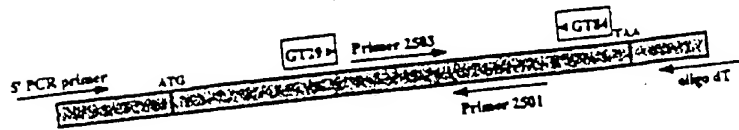


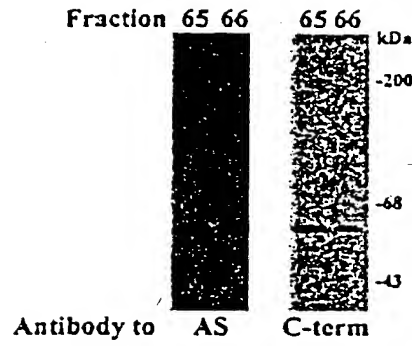
Fig. 3

MEXKISFLIYSLISANSRD-KGKNKINNSLGI IRENKNKTHQTEIHE 50
 SFSHLKSNNHNFVEYSGYCGGCGNSRIITKNNKNINKNCRKSPRGILEEYK 100
 KRKGGIAGTYGSWNSGCCRAKHNIOSNPHYSILYIAFARINMLYQVSRP 150
 FNGCRFLLRKHGLEYYTGMHLEIRRIKVRPOVILLSTGETYHID 200
 IEKEIDYYOKILKLYNC ^{Substrate binding site} HGKFYNLNLNFSNYYIKLIN 250
 LLRKTPEEKLISIGSSNAALSCVSGVASFCXDEESPYNKFLSEQIET 300
 NKELHRAAAMLSAGTFINIFNTAKEIOLYFIQTYNLETTNPDIHVCHYL 350
 SHLYPGLKYNITILGFSLEHNRGCFSPENKELLELYCKT(HOKNCHNMR 400
 AOGIGIWHLFMKEQLPTGSOVDIFLTNIW ^{Catalytic active site} HLPYQTPDOLTITENPE 450
 OCSTIDEYYPGLVIPTIGIYYKHNGAIWKTRSYSIHAPGVORYEGLVKY 500
 CYEXICCGK ^{Catalytic active site} HAHYYNIDYKSSIIWKCEPYLIKWCCPPGQALESYT 550
 KLEASKCPGIEWNKKY ^{Catalytic active site} PHKPLEYEEQTEQEVOLPLQ 587

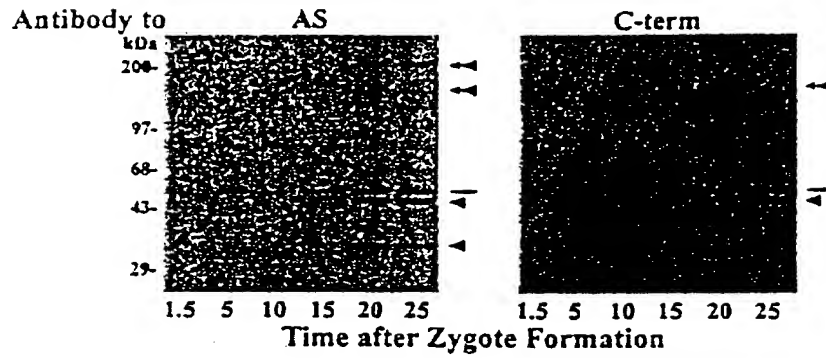
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Fig. 4

a



b



c

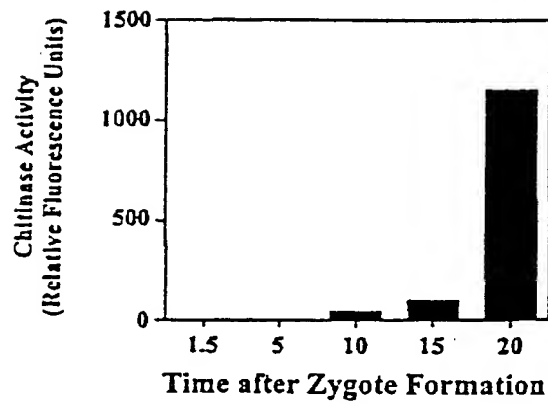


Fig. 5

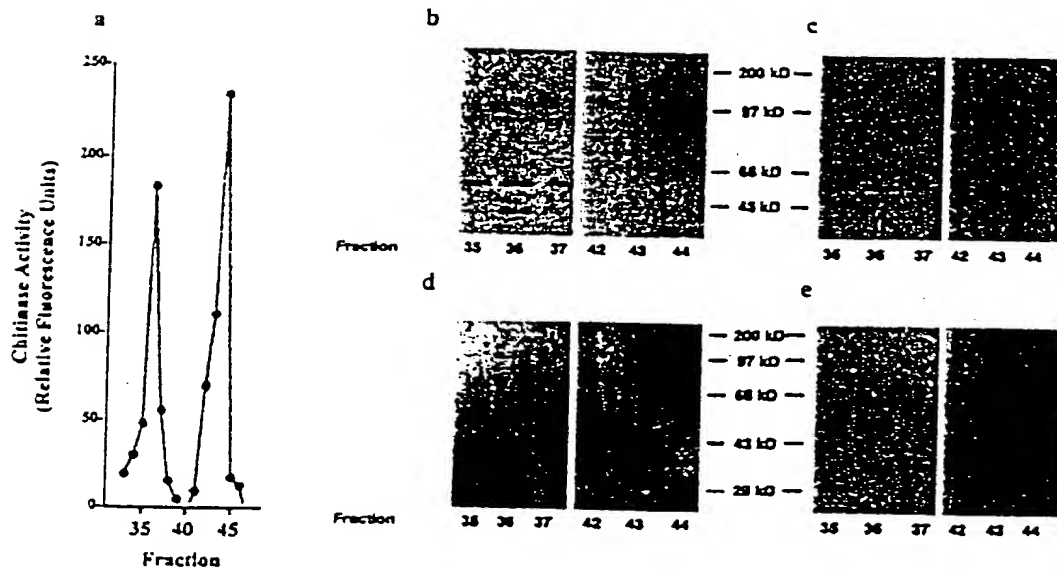


Fig. 6

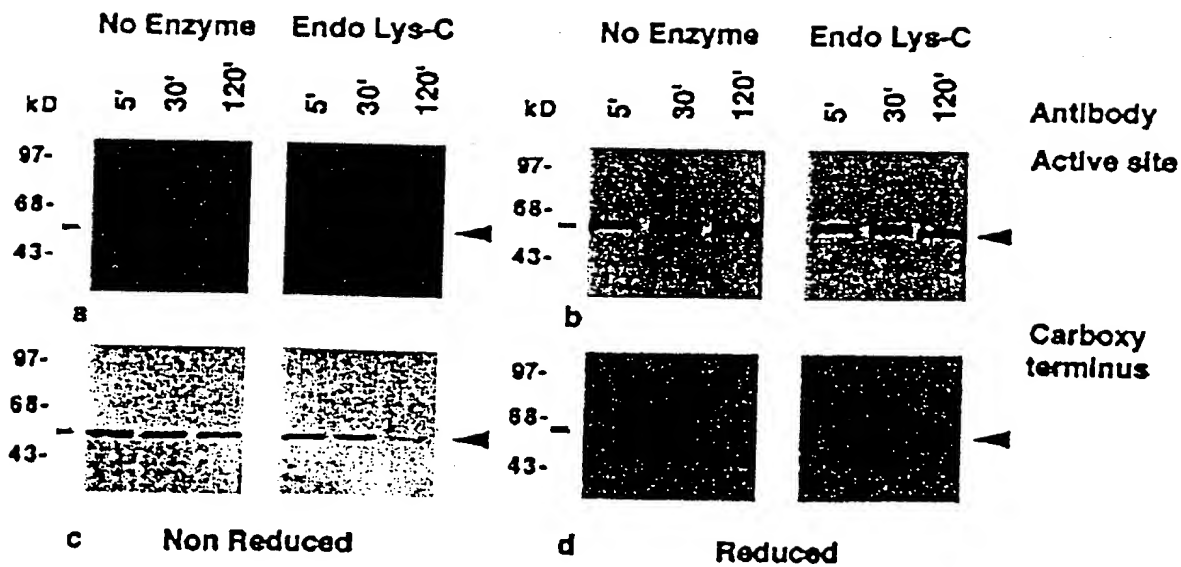


Fig. 7

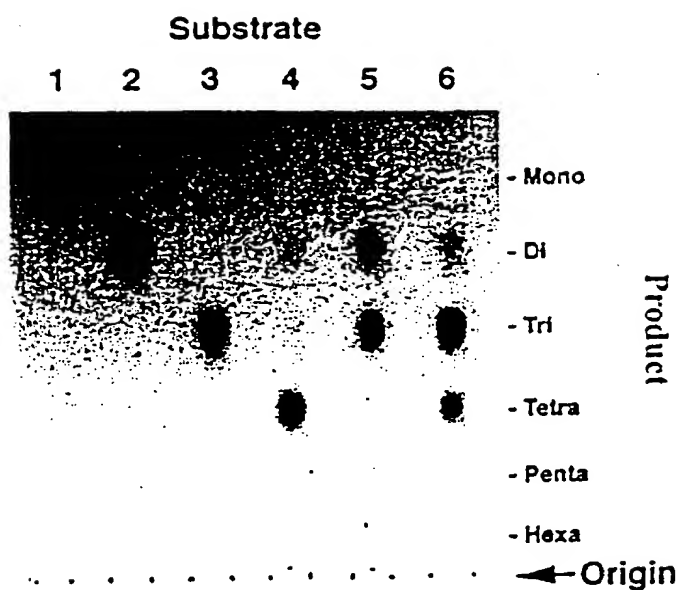
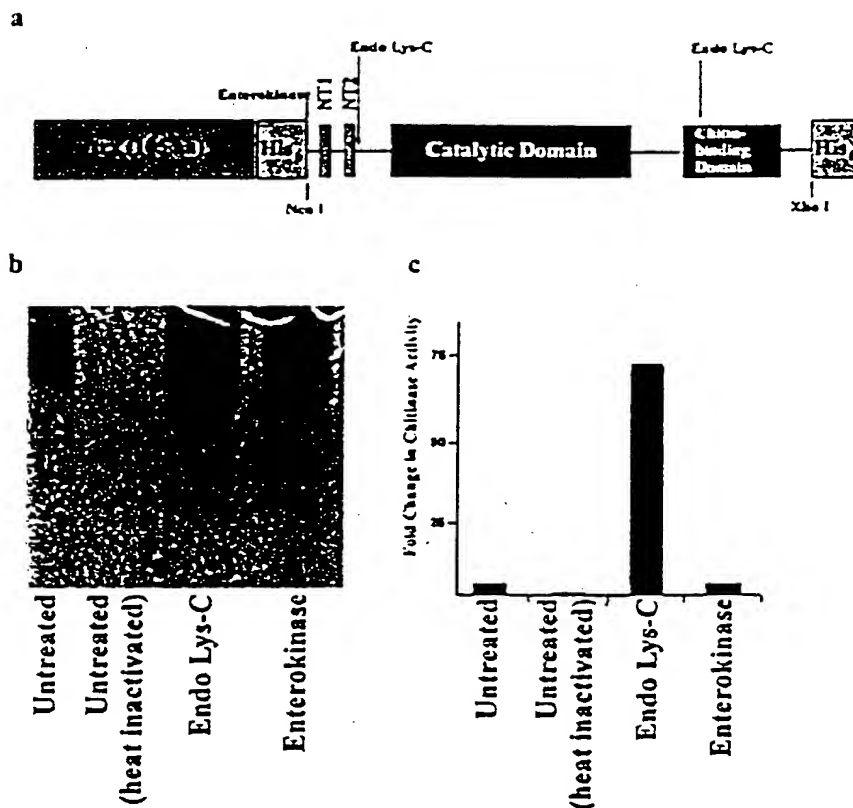


Fig. 8

Fig. 9

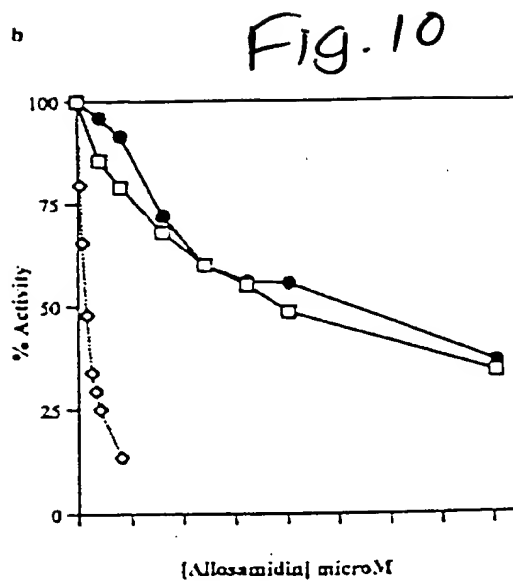
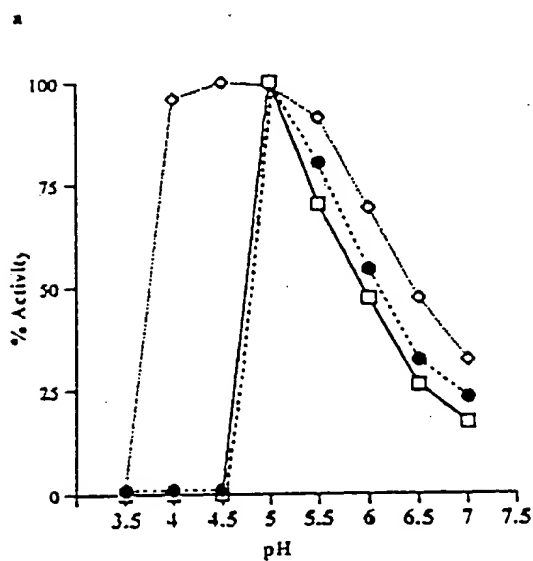
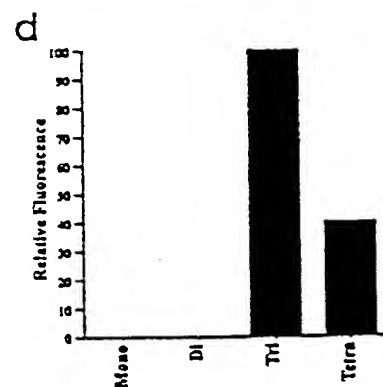
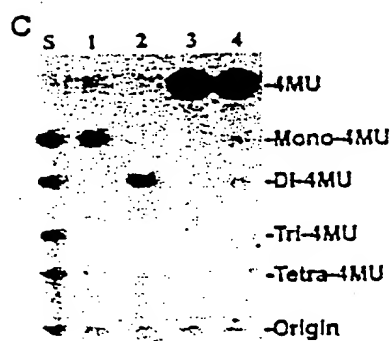
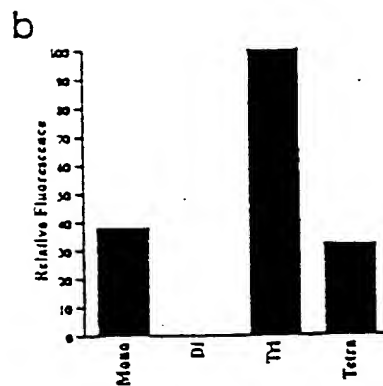
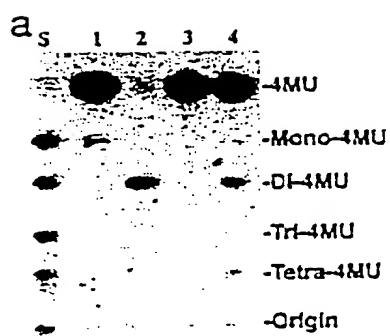


Fig. 11

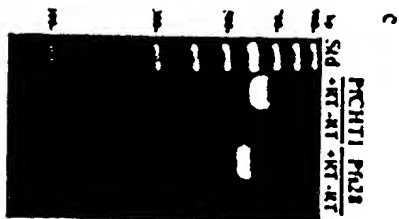
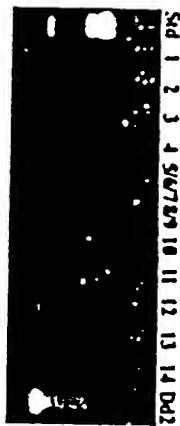
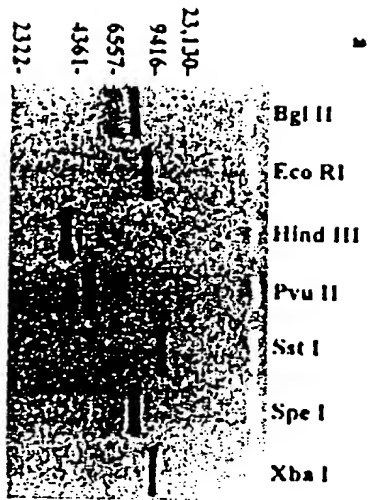
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PgCMT1  METVKSPLVAGLACGLSTVSVIEG----- 28
PgCMT1  KATKISLELVSVLSANSRI-----Proteinase domain
                                         AKGNINNSLDILPENNQNHQTEHRSFSHLKSNNSNCE 64

PgCMT1  HBARPGESR-----Catalytic domain begins
                                         PRRIKTPRESGKILQGYTPSWSYNRHLDL- 72
                                         **:::**:*** ** * * *
PgCMT1  -----VGYCGDCGNSRIITQNTQINIDRKSPQILLETQOKQQLIAGTYGSMNSQGDRADEMY 125
                                         NT1      NT2
                                         Substrate-binding
                                         site
PgCMT1  --NPNLVNVPASPAQDLSYDSIESIVGSPLLFKSLIGLETYIGLNEYNDANLRAAPDIIHLLSLQGR 140
                                         **:::**:*** ** * * *
PgCMT1  DSNPVSILYIAFAINMLYDVSRRPNQRQRLBEGLEETTYGGLNEIRIRIKVRPDVILLSLQGR 195
                                         **:::**:*** ** * * *
PgCMT1  TMAPSSFDNALNAVZKIANLVDELQFDQIDVDYEPNQSFDQNDKEKADFVQVYTKLRETHCDNLISI 210
                                         Active site
                                         **:::**:*** ** * * *
PgCMT1  TTM-IDIRKEIDVDKILKLVNDFDLDQVDIDWEPHQKFTNLNLPNSNYIKLINLAKTIPEKILSI 264
                                         **:::**:*** ** * * *
PgCMT1  SSSNCAALSCI-GPNDPKICQDDEAFVNSKYYNKP-DVKKELLRAQHASAGQAIYLPANLQCHIDMV 278
                                         ****::*** ** * * *
PgCMT1  SSSNALSVCVSGVAS--PCDRESPTNKTLSQIETKSELBAALSLAGTPINIPNTAKCKIDLVP 331
                                         ****::*** ** * * *
PgCMT1  VQTPNNTNSTDSVMGELVDSVAYGKRYDVIIHCFLLAPPSTPNPNDRLVKSIGDPVKTENKLANR 348
                                         **:::**:*** ** * * *
PgCMT1  IOTNVL-ETINPDIMDMYLSHLVFGLNITITILGFSLEHNRGCFSPENKELLELVGKTIHDNQNQNR 400
                                         **:::**:*** ** * * *
PgCMT1  ADGFGLSLSDDRAARHQLAIRTVESLH. 378Catalytic domain ends
                                         ADGFGLSLSDDRAARHQLAIRTVESLH. 378
                                         ****::*** ** * * *
PgCMT1  ADGIGIWHLPNKEQLPTGSPDVIDFLTNMKHLNPEVQTPKDLITTENPDCSTIDETVPGLVITIGIN 470
                                         ****::*** ** * * *
PgCMT1  DYYKHALNKRISYSIHAPGVDRVMDLVNVCYEKICDGRKATNTDYKASSIILNKGEPYLIRNMQGP 540
PgCMT1  PEGQALSYYTLDAASKCPQIBENNKYPPHPLAVEBQYBQBDLPQ. 587
                                         ****::*** ** * * *
                                         Chitin-binding domain
                                         begins

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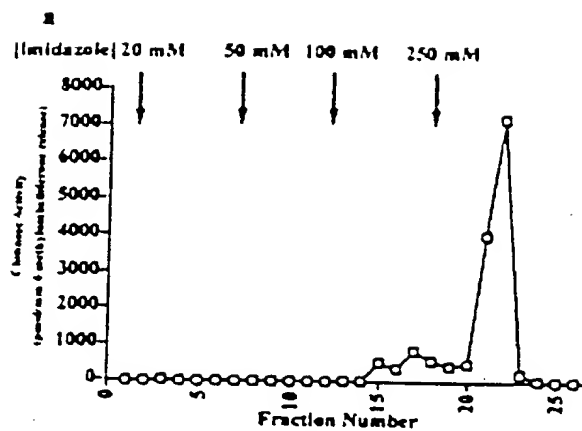
Fig. 12



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Fig. 13



b

c

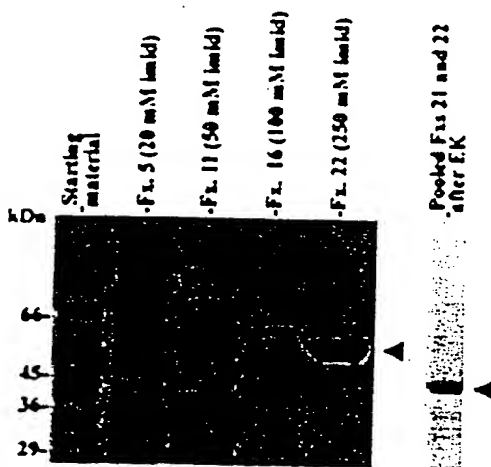
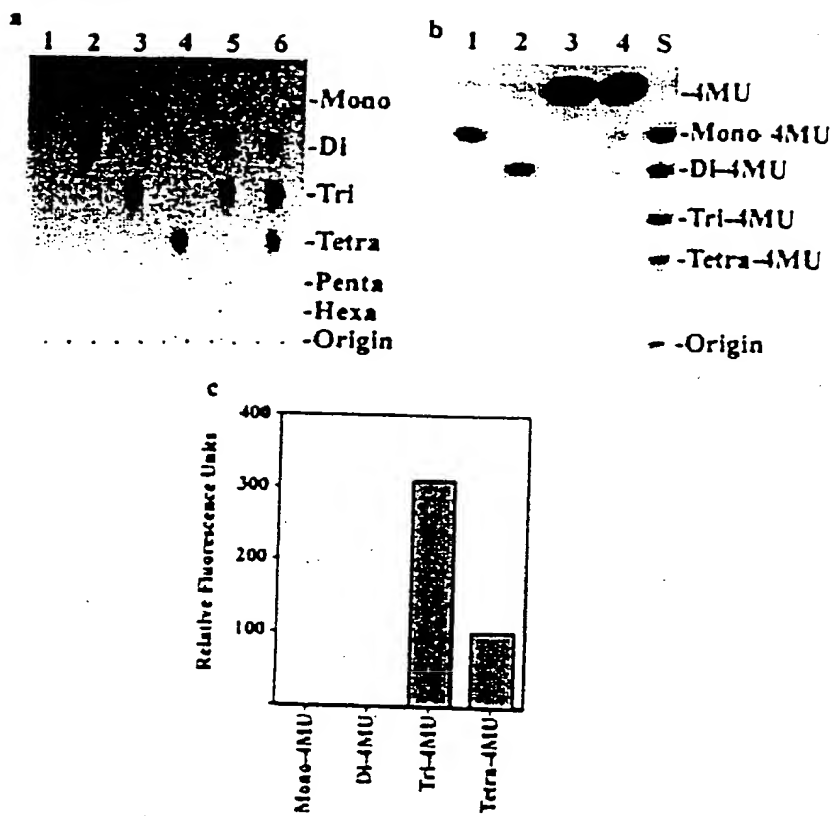


Fig. 14



009250" E8E6/560

Fig. 15

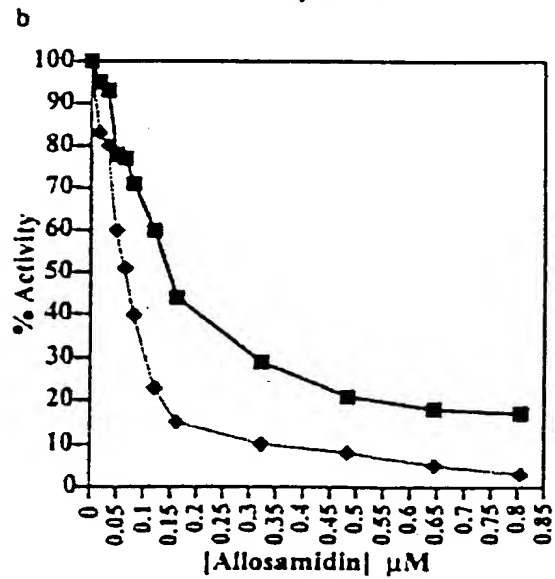
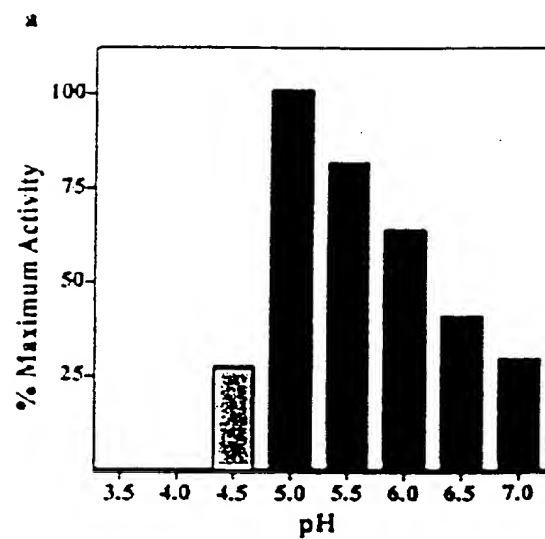


Fig. 16



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